1. (Twice amended) A method for determining the type of target nucleic acids in a sample, wherein the method is capable of differentiating free and encapsulated target nucleic acids in the sample, wherein the method comprises

(a) determining a total target nucleic acid content in the sample;

(b) adding a nuclease to the sample to digest free target nucleic acids in the sample to form a nuclease-treated sample;

(c) determining a total target nucleic acid content remaining in the nuclease-treated sample, thereby quantifying the amount of encapsulated target nucleic acids in the sample; and

(d) quantifying the total amount of free target nucleic acid in the sample by subtracting the determined amount of target nucleic acid content in the nuclease-treated sample from the determined amount of total target nucleic acid content in the sample, wherein steps (c) and (d) determine the types of target nucleic acids in the sample.

3. (Twice amended) The method of claim 1, wherein all determining of the target nucleic acids is performed using a nucleic acid amplification assay selected from the group consisting of a polymerase chain reaction (PCR) assay and a reverse transcriptase (RT) PCR assay.

21. (Amended) A method for determining the proportion of infectious pathogens and inactivated pathogens in a sample, wherein the method is capable of

differentiating free and encapsulated target nucleic acids in the sample, wherein the method comprises

(a) determining a total target nucleic acid content in the sample;

(b) adding a nuclease to the sample to digest free target nucleic acids in the sample to form a nuclease-treated, wherein the nuclease will not digest the encapsulated target nucleic acids;

(c) determining a total target nucleic acid content remaining undigested in the nuclease-treated sample, which represents the amount of infectious pathogens in the sample;

(d) quantifying the total amount of free target nucleic acid in the sample by subtracting the determined amount of undigested target nucleic acid content in the nuclease-treated sample from the determined amount of total target nucleic acid content in the sample, wherein the quantifying indicates the amount of inactivated pathogens in the sample; and

(e) comparing the amounts from steps (c) and (d) to determine the proportion of infectious pathogens and inactivated pathogens in the sample.

23. (Amended) The method of claim 21, wherein all determining of the target nucleic acids is performed using a nucleic acid amplification assay selected from the group consisting of a polymerase chain reaction (PCR) assay and a reverse transcriptase (RT) PCR assay.

31. (Amended) A method for detecting infectious pathogens in a sample, wherein the method comprises

(a) determining a total target nucleic acid content in the sample;

(b) adding a nuclease to the sample to digest any free target nucleic acids in the sample to form a nuclease-treated sample, wherein the nuclease will not digest the encapsulated target nucleic acids; and

(c) detecting infectious pathogens that may be present in the sample by determining a total target nucleic acid content remaining in the nuclease-treated sample, which represents the amount of infectious pathogens in the sample.

33. (Amended) The method of claim 31, wherein all determining of the target nucleic acids is performed using a nucleic acid amplification assay selected from the group consisting of a polymerase chain reaction (PCR) assay and a reverse transcriptase (RT) PCR assay.

42. (New) The method of claim 31, wherein samples that have acceptable levels of infectious pathogens are used for the preparation of biological products.

43. (New) The method of claim 31, wherein samples that have unacceptable levels of infectious pathogens are discarded or subjected to at least one of a pathogen inactivation treatment or a pathogen removal treatment.